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IN THE CLAIMS

Please cancel claims 2 and 12 without prejudice or disclaimer.

Please amend claims 1 and 3 as follows (*a marked up copy of the amended claims is provided as an Appendix to this Response*):

C1
1. (Twice Amended) A method of predicting a scaffold of a protein comprising a query sequence, wherein said method uses a database which contains environmental information on the side chain of each amino acid residue contained in the amino acid sequence of each reference protein whose three-dimensional structure is predetermined, and wherein said method comprises: conducting matching based on the environmental information of each amino acid residue of each reference protein and hydrophobicity or hydrophilicity property of the side chain of each amino acid residue of the query sequence, choosing at least one protein as a template protein from the reference proteins that has high similarity in three-dimensional structure to the protein comprising the query sequence, and predicting the scaffold of the protein comprising a query sequence, wherein the amino acid sequence of each of the reference proteins is divided into two or more segment sequences comprising two or more continuous amino acid residues based on the characteristics of the three-dimensional structure of the reference protein.

C2
3. (Twice Amended) The method according to claim 1, wherein the amino acid sequence of each of the reference proteins is divided into one or more core segment sequences which are